

TRANSLATION OF PRIORITY DOCUMENT OF CN02145253.9

SEQUENCE LISTING

<110> SHANGHAI INSTITUTES FOR BIOLOGICAL SCIENCES, CAS

<120> METHOD OF DIAGNOSING AND TREATING BALDNESS USING HUMAN AND MOUSE RHOR GENE AND CODED PRODUCT THEREOF

<130> 026816

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 2484

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (1)..(2481)

<223>

<400> 1

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Met	Ala	Ser	Ala	Asp	Lys	Asn	Gly	Ser	Asn	Leu	Pro	Ser	Val	Ser	Gly	
1	5					10				15						

agc	cgc	ctg	cag	agc	cgg	aag	cca	ccc	aac	ctc	tcc	atc	acc	atc	ccg	96
Ser	Arg	Leu	Gln	Ser	Arg	Lys	Pro	Pro	Asn	Leu	Ser	Ile	Thr	Ile	Pro	
20	25					30										

cca	cca	gag	agc	cag	gcc	ccc	ggc	gag	cag	gat	agc	atg	ctt	cct	gag	144
Pro	Pro	Glu	Ser	Gln	Ala	Pro	Gly	Glu	Gln	Ser	Met	Leu	Pro	Glu		
35	40					45										

agg	cgc	aag	aac	cca	gcc	tac	ctg	aag	agt	gtc	agc	cta	cag	gag	ccc	192
Arg	Arg	Lys	Asn	Pro	Ala	Tyr	Leu	Lys	Ser	Val	Ser	Leu	Gln	Glu	Pro	
50	55					60										

cgg	gga	cga	tgg	cag	gag	ggc	gca	gag	aag	cgc	ccc	ggc	ttc	cgc	cgc	240
Arg	Gly	Arg	Trp	Gln	Glu	Gly	Ala	Glu	Lys	Arg	Pro	Gly	Phe	Arg	Arg	
65	70			75		80										

cag	gcc	tcc	ctg	tcc	cag	agc	atc	cgc	aag	agc	aca	gcc	cag	tgg	ttt	288
Gln	Ala	Ser	Leu	Ser	Gln	Ser	Ile	Arg	Lys	Ser	Thr	Ala	Gln	Trp	Phe	
85	90			95												

ggg	gtc	agc	ggc	gac	tgg	gag	ggc	aag	cga	caa	aac	tgg	cat	cgt	cgc	336
Gly	Val	Ser	Gly	Asp	Trp	Glu	Gly	Lys	Arg	Gln	Asn	Trp	His	Arg	Arg	
100	105			110												

agc	ctg	cac	tgc	agc	gtg	cac	tat	ggc	cgc	ctc	aag	gcc	tcg	tgc	384	
Ser	Leu	His	His	Cys	Ser	Val	His	Tyr	Gly	Arg	Leu	Lys	Ala	Ser	Cys	
115	120			125												

cag	aga	gaa	ctg	gag	ctg	ccc	agc	cag	gag	gtg	cca	tcc	tcc	cag	ggc	432
Gln	Arg	Glu	Leu	Glu	Leu	Pro	Ser	Gln	Glu	Val	Pro	Ser	Phe	Gln	Gly	
130	135			140												

act	gag	tct	cca	aaa	ccg	tgc	aag	atg	ccc	aag	att	gtg	gat	cca	ctg	480
Thr	Glu	Ser	Pro	Lys	Pro	Cys	Lys	Met	Pro	Lys	Ile	Val	Asp	Pro	Leu	
145	150			155							160					

gct	cggt	agg	gcc	ttc	cgc	cat	cca	gat	gag	gtg	gac	cg	cct	cac		528
Ala	Arg	Arg	Ala	Phe	Arg	His	Pro	Asp	Glu	Val	Asp	Arg	Pro	His		
165	170			175												

gct	gcc	cac	cca	cct	ctg	act	cca	ggg	gtc	ctg	tct	ctc	aca	tcc	tcc	576
Ala	Ala	His	Pro	Pro	Leu	Thr	Pro	Gly	Val	Leu	Ser	Leu	Thr	Ser	Phe	

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180	185	190	
acc agt gtc cgc tct ggc tac tcc cat ctg ccc cgc cgc aag agg ata			624
Thr Ser Val Arg Ser Gly Tyr Ser His Leu Pro Arg Arg Lys Arg Ile			
195	200	205	
tct gtt gcc cat atg agc ttt cag gca gcc gcc ctc ctc aag ggg			672
Ser Val Ala His Met Ser Phe Gln Ala Ala Ala Leu Leu Lys Gly			
210	215	220	
cgt tcc gtg cta gat gcg act ggg cag cgg tgc cgg cat gtc aaa cgc			720
Arg Ser Val Leu Asp Ala Thr Gly Gln Arg Cys Arg His Val Lys Arg			
225	230	235	240
agc ttc gct tac ccc agc ttc ctg gag gag gat gct gtc gat gga gct			768
Ser Phe Ala Tyr Pro Ser Phe Leu Glu Glu Asp Ala Val Asp Gly Ala			
245	250	255	
gac acc ttc gac tcc tcc ttt agt aag gaa gaa atg agc tcc atg			816
Asp Thr Phe Asp Ser Ser Phe Phe Ser Lys Glu Glu Met Ser Ser Met			
260	265	270	
cct gac gat gtc ttt gag tcc ccc cca ctc tct gcc agc tac ttc cga			864
Pro Asp Asp Val Phe Glu Ser Pro Pro Leu Ser Ala Ser Tyr Phe Arg			
275	280	285	
ggt gtc cca cac tct gcc tcc ccg gtc tcc ccg gat gga gtg cac atc			912
Gly Val Pro His Ser Ala Ser Pro Val Ser Pro Asp Gly Val His Ile			
290	295	300	
ccg cta aaa gaa tac agc ggt ggc cga gcc ctg ggt ccc ggg acc cag			960
Pro Leu Lys Glu Tyr Ser Gly Gly Arg Ala Leu Gly Pro Gly Thr Gln			
305	310	315	320
cgt ggc aaa cgc att gcc tcc aaa gta aag cac ttt gca ttt gac cgg			1008
Arg Gly Lys Arg Ile Ala Ser Lys Val Lys His Phe Ala Phe Asp Arg			
325	330	335	
aag aag agg cac tac ggc ctg ggt gtc gtg ggt aac tgg ctc aac cga			1056
Lys Lys Arg His Tyr Gly Leu Gly Val Val Gly Asn Trp Leu Asn Arg			
340	345	350	
agc tat cga cgc agc atc agc acc gtg cag cgg cag ctg gag agc			1104
Ser Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln Arg Gln Leu Glu Ser			
355	360	365	
ttc gat agc cac cgg ccc tac ttc acc tac tgg ctg acg ttc gtt cac			1152
Phe Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp Leu Thr Phe Val His			
370	375	380	
atc atc atc acc ttg ctg gtg atc tgc acc tat ggc atc atc gca cct gtg			1200
Ile Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr Gly Ile Ala Pro Val			
385	390	395	400
ggc ttt gcc cag cac gtt acc acc cag ctg gtg ctg aag aac aac aga ggc			1248
Gly Phe Ala Gln His Val Thr Thr Gln Leu Val Leu Lys Asn Arg Gly			
405	410	415	
gtg tat gag agc gtg aag tac atc cag cag gag aac ttc tgg att ggc			1296
Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Ile Gly			
420	425	430	
ccc agc tcg att gac ctc att cac ctg gga gca aag ttc tcg ccc tgc			1344
Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys			
435	440	445	
atc cgg aag gac cag caa att gag cag ctg gta cgg agg gag gag cgc gac			1392
Ile Arg Lys Asp Gln Gln Ile Glu Gln Leu Val Arg Arg Glu Arg Asp			
450	455	460	
att gag cgc acc tct ggc tgc tgt gtc cag aat gac cgc tcg ggc tgc			1440
Ile Glu Arg Thr Ser Gly Cys Cys Val Gln Asn Asp Arg Ser Gly Cys			
465	470	475	480
atc cag acc ctg aag aag gac tgc tcg gag act tta gcc acg ttc gta			1488
Ile Gln Thr Leu Lys Lys Asp Cys Ser Glu Thr Leu Ala Thr Phe Val			
485	490	495	
aag tgg cag aat gat act ggg ccc tca gac aag tct gac ctg agc cag			1536

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Lys Trp Gln Asn Asp Thr Gly Pro Ser Asp Lys Ser Asp Leu Ser Gln			
500	505	510	
aag cag cca tcg gcg gtt gtg tgc cac caa gac ccc agg acc tgt gaa			1584
Lys Gln Pro Ser Ala Val Val Cys His Gln Asp Pro Arg Thr Cys Glu			
515	520	525	
gag cct gcc tcc agt ggg gcc cac atc tgg cct gat gac att acc aag			1632
Glu Pro Ala Ser Ser Gly Ala His Ile Trp Pro Asp Asp Ile Thr Lys			
530	535	540	
tgg ccg atc tgc aca gag cag gct cag agc aac cac acg ggc ttg ttg			1680
Trp Pro Ile Cys Thr Glu Gln Ala Gln Ser Asn His Thr Gly Leu Leu			
545	550	555	560
cac ata gac tgt aag atc aaa ggc cgc ccc tgc tgc atc ggc acc aag			1728
His Ile Asp Cys Lys Ile Lys Gly Arg Pro Cys Cys Ile Gly Thr Lys			
565	570	575	
ggc agc tgc gag atc acc act cgg gag tac tgt gag ttc atg cat ggc			1776
Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr Cys Glu Phe Met His Gly			
580	585	590	
tat ttc cat gaa gac gcg acg ctg tgt tcc cag gtg cac tgt tta gac			1824
Tyr Phe His Glu Asp Ala Thr Leu Cys Ser Gln Val His Cys Leu Asp			
595	600	605	
aag gtg tgt ggg ctc ctg cct ttc ctc aac cct gag gtc cct gac cag			1872
Lys Val Cys Gly Leu Leu Pro Phe Leu Asn Pro Glu Val Pro Asp Gln			
610	615	620	
ttc tac cgg atc tgg ctg tct tta ttc ctg cat gct ggc ata gtg cac			1920
Phe Tyr Arg Ile Trp Leu Ser Leu Phe Leu His Ala Gly Ile Val His			
625	630	635	640
tgc ctt gtg tct gtg gtc ttc caa atg acc atc ctg agg gac cta gag			1968
Cys Leu Val Ser Val Val Phe Glu Met Thr Ile Leu Arg Asp Leu Glu			
645	650	655	
aag ctg gcc ggc tgg cac cgc atc tcc atc atc ttc atc ctt agt ggc			2016
Lys Leu Ala Gly Trp His Arg Ile Ser Ile Ile Phe Ile Leu Ser Gly			
660	665	670	
att aca ggc aac ctg gcc agc gcc atc ttc ctc ccc tac cgg gca gag			2064
Ile Thr Gly Asn Leu Ala Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu			
675	680	685	
gtg ggc cca gcc ggg tcg cag ttc ggc ctc ctc gcc tgc ctc ttc gtg			2112
Val Gly Pro Ala Gly Ser Gln Phe Gly Leu Leu Ala Cys Leu Phe Val			
690	695	700	
gag ctg ttc cag agc tgg cag ctg ttg gag cgg cgg tgg aag gcc ttc			2160
Glu Leu Phe Gln Ser Trp Gln Leu Leu Glu Arg Pro Trp Lys Ala Phe			
705	710	715	720
ttc aac ctg tcg gcc att gtg ctt ttc ctc ttc atc tgt ggc ctc ctg			2208
Phe Asn Leu Ser Ala Ile Val Leu Phe Leu Phe Ile Cys Gly Leu Leu			
725	730	735	
ccc tgg ata gac aac atc gcc cac atc ttc ggg ttc ctc agc ggc atg			2256
Pro Trp Ile Asp Asn Ile Ala His Ile Phe Gly Phe Leu Ser Gly Met			
740	745	750	
ctt ctg gcc ttc gcc ttc ctg cct tac att acc ttc ggc acc agc gac			2304
Leu Leu Ala Phe Ala Phe Leu Pro Tyr Ile Thr Phe Gly Thr Ser Asp			
755	760	765	
aag tac cgc aag cga gcc ctc atc ctc gtg tcg ctg ctg gtc ttt gct			2352
Lys Tyr Arg Lys Arg Ala Leu Ile Leu Val Ser Leu Leu Val Phe Ala			
770	775	780	
ggg ctc ttt gct tcc ctg gtg ctg tgg ctg tac atc tac ccc atc aac			2400
Gly Leu Phe Ala Ser Leu Val Leu Trp Leu Tyr Ile Tyr Pro Ile Asn			
785	790	795	800
tgg ccc tgg atc gag tac ctc acc tgc ttt ccc ttc acc agc cgc ttc			2448
Trp Pro Trp Ile Glu Tyr Leu Thr Cys Phe Pro Phe Thr Ser Arg Phe			
805	810	815	

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tgt gag aag tac gag cta gac cag gtg cta cac taa 2484
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 820 825

<210> 2
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 <212> PRT
 <213> Mus musculus

<400> 2

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 Pro Pro Glu Ser Gln Ala Pro Gly Glu Gln Asp Ser Met Leu Pro Glu
 35 40 45
 Arg Arg Lys Asn Pro Ala Tyr Leu Lys Ser Val Ser Leu Gln Glu Pro
 50 55 60
 Arg Gly Arg Trp Gln Glu Gly Ala Glu Lys Arg Pro Gly Phe Arg Arg
 65 70 75 80
 Gln Ala Ser Leu Ser Gln Ser Ile Arg Lys Ser Thr Ala Gln Trp Phe
 85 90 95
 Gly Val Ser Gly Asp Trp Glu Gly Lys Arg Gln Asn Trp His Arg Arg
 100 105 110
 Ser Leu His His Cys Ser Val His Tyr Gly Arg Leu Lys Ala Ser Cys
 115 120 125
 Gln Arg Glu Leu Glu Leu Pro Ser Gln Glu Val Pro Ser Phe Gln Gly
 130 135 140
 Thr Glu Ser Pro Lys Pro Cys Lys Met Pro Lys Ile Val Asp Pro Leu
 145 150 155 160
 Ala Arg Gly Arg Ala Phe Arg His Pro Asp Glu Val Asp Arg Pro His
 165 170 175
 Ala Ala His Pro Pro Leu Thr Pro Gly Val Leu Ser Leu Thr Ser Phe
 180 185 190
 Thr Ser Val Arg Ser Gly Tyr Ser His Leu Pro Arg Arg Lys Arg Ile
 195 200 205
 Ser Val Ala His Met Ser Phe Gln Ala Ala Ala Leu Leu Lys Gly
 210 215 220
 Arg Ser Val Leu Asp Ala Thr Gly Gln Arg Cys Arg His Val Lys Arg
 225 230 235 240
 Ser Phe Ala Tyr Pro Ser Phe Leu Glu Glu Asp Ala Val Asp Gly Ala
 245 250 255
 Asp Thr Phe Asp Ser Ser Phe Phe Ser Lys Glu Glu Met Ser Ser Met
 260 265 270
 Pro Asp Asp Val Phe Glu Ser Pro Pro Leu Ser Ala Ser Tyr Phe Arg
 275 280 285
 Gly Val Pro His Ser Ala Ser Pro Val Ser Pro Asp Gly Val His Ile
 290 295 300
 Pro Leu Lys Glu Tyr Ser Gly Gly Arg Ala Leu Gly Pro Gly Thr Gln
 305 310 315 320
 Arg Gly Lys Arg Ile Ala Ser Lys Val Lys His Phe Ala Phe Asp Arg
 325 330 335
 Lys Lys Arg His Tyr Gly Leu Gly Val Val Gly Asn Trp Leu Asn Arg
 340 345 350
 Ser Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln Arg Gln Leu Glu Ser
 355 360 365
 Phe Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp Leu Thr Phe Val His
 370 375 380

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Ile Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr Gly Ile Ala Pro Val
 385 390 395 400
 Gly Phe Ala Gln His Val Thr Thr Gln Leu Val Leu Lys Asn Arg Gly
 405 410 415
 Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Ile Gly
 420 425 430
 Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys
 435 440 445
 Ile Arg Lys Asp Gln Gln Ile Glu Gln Leu Val Arg Arg Glu Arg Asp
 450 455 460
 Ile Glu Arg Thr Ser Gly Cys Cys Val Gln Asn Asp Arg Ser Gly Cys
 465 470 475 480
 Ile Gln Thr Leu Lys Lys Asp Cys Ser Glu Thr Leu Ala Thr Phe Val
 485 490 495
 Lys Trp Gln Asn Asp Thr Gly Pro Ser Asp Lys Ser Asp Leu Ser Gln
 500 505 510
 Lys Gln Pro Ser Ala Val Val Cys His Gln Asp Pro Arg Thr Cys Glu
 515 520 525
 Glu Pro Ala Ser Ser Gly Ala His Ile Trp Pro Asp Asp Ile Thr Lys
 530 535 540
 Trp Pro Ile Cys Thr Glu Gln Ala Gln Ser Asn His Thr Gly Leu Leu
 545 550 555 560
 His Ile Asp Cys Lys Ile Lys Gly Arg Pro Cys Cys Ile Gly Thr Lys
 565 570 575
 Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr Cys Glu Phe Met His Gly
 580 585 590
 Tyr Phe His Glu Asp Ala Thr Leu Cys Ser Gln Val His Cys Leu Asp
 595 600 605
 Lys Val Cys Gly Leu Leu Pro Phe Leu Asn Pro Glu Val Pro Asp Gln
 610 615 620
 Phe Tyr Arg Ile Trp Leu Ser Leu Phe Leu His Ala Gly Ile Val His
 625 630 635 640
 Cys Leu Val Ser Val Val Phe Gln Met Thr Ile Leu Arg Asp Leu Glu
 645 650 655
 Lys Leu Ala Gly Trp His Arg Ile Ser Ile Ile Phe Ile Leu Ser Gly
 660 665 670
 Ile Thr Gly Asn Leu Ala Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu
 675 680 685
 Val Gly Pro Ala Gly Ser Gln Phe Gly Leu Leu Ala Cys Leu Phe Val
 690 695 700
 Glu Leu Phe Gln Ser Trp Gln Leu Leu Glu Arg Pro Trp Lys Ala Phe
 705 710 715 720
 Phe Asn Leu Ser Ala Ile Val Leu Phe Leu Phe Ile Cys Gly Leu Leu
 725 730 735
 Pro Trp Ile Asp Asn Ile Ala His Ile Phe Gly Phe Leu Ser Gly Met
 740 745 750
 Leu Leu Ala Phe Ala Phe Leu Pro Tyr Ile Thr Phe Gly Thr Ser Asp
 755 760 765
 Lys Tyr Arg Lys Arg Ala Leu Ile Leu Val Ser Leu Leu Val Phe Ala
 770 775 780
 Gly Leu Phe Ala Ser Leu Val Leu Trp Leu Tyr Ile Tyr Pro Ile Asn
 785 790 795 800
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 Cys Glu Lys Tyr Glu Leu Asp Gln Val Leu His
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<211> 20

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ccagtggttt ggggtcagcg cgcgactggga gggcaagcga caaaactggc atcgtcgccag 180
cctgcaccac tgcagcgtgc actatggccg cctcaaggcc tcgtgccaga gagaactgg 240
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tcagcggcga ctggggggc aagcgacaaa actggcatcg tcgcggcctg caccactgca	180	
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atccactggc tgggggttagg gccttccggc atccagatga ggtggaccgg cctcacgt	360	
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cgccgcctc ctcaggggc gttccgtgt agatgcgact gggcagcgt gcccgcgt	540	
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